



SEQUENCE LISTING

1

<12 >> PRODUCTION OF ADENINE NUCLEOTIDE
 THANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 THEREFOR

<130> 660088.420

<1405 US 39/195,904

<141> 1998-11-03

<160> 33

<170> FastSEO for Windows Version 3.0

<210> 1

<..11> 594

<.:12> DNA

<213> Homo sapien

<4.00>-1

atgggtgatc	adgottggag	ottootaaag	gadttddtgg	cagagagaggt	agaagatgaa	60
gtotocaaga	pagaggtaga	deceatogag	agggtcaaac	tgotgotgoa	ggtddagdat	120
godagdanad	agatcagtgo	tgagaagcag	tacaaaggga	toattgattg	tgtggtgaga	180
atccctaagg	agcagggctt	actateatta	tggaggggta	acctggccaa	cgtgatccgt	240
tabttbbbba	promangetet	daadttogdo	ttcaaggaca	agtacaagca	gotottotta	3 10
3333323,33	atoggoataa	gdagttdtgg	agetactttg	otggtaacct	ggagtaaggt	300
ggggaagatq	gggadaaata	actitigatit	gtotacccgo	tggactttgc	taggadbagg	400
ttggatguta	atutgggcag	gogogoddag	ogtgagttod	atggtotggg	cgactgtatc	$4 \approx 0$
atcaagatot	traagtotga	tggddtgagg	gggatataaa	agggtttdaa	agtatatgta	540
caaggcatca	tratostatag	agotgootad	ttoggagtet	atgatactgo	daaggggatg	6,10
otgootgass	ренадаврус	gdadattfft	grigagorigga	tgattgccca	gagtgtgacg	らくか
gdagtog rad	ggatgatgta	stassettt	gacactgttc	gtogtagaat	gatgatgdag	7.1.0
tdoggoogga	ааддддссда	tattatgtac	acggggacag	ttgadtgdtg	gaggaagatt	760
дсававдисд	aaggagodaa	ggoottotto	aaaggtgoot	ggtccaatgt	gotgagaggo	840
atgggcggtg	dthttgtatt	ggtgttgtat	gatgagatca	aaaaatatgt	ctaa	8 14

<.105 2

<211> 337

<1113 DMA

<113> Homo sapien

<400> 2

atgacagatg objecting obtogodaag gabttootgg baggtggagt ggbgbagdd 50 atotobaaga oggogatago goddathgag hgggfhaago tgotgotgda ggtgbagdat 120 gobagdaago agatbactgd agataagdaa tadaaaggda ttatagabtg bgtggthogt 180

```
attoccaagg agcaggaagt totgtootto toggogoggta acctggccaa togtoatcaga
                                                                                                                                        240
                                                                                                                                        3:00
tacticocca occaggetut Laacticocc tibaaaagata aatacaagca gatottooto
                                                                                                                                        360
ggtggtgtgg acaagagaac ccagttttgg cgctactttg cagggaatct ggcatcgggt
                                                                                                                                        420
ggtgeegeag gggeeacate betgtgtttt gtgtadeete ttgattttgd begtadeegt.
stagsagstg atgtgggtaa agdrggagst gaaaggqaat tocgaggsst oggtgastgs
                                                                                                                                        480
obggbbaaga bobacaaabo bgabgggabb aagggcobgb accaaggobb baacgbgbch
                                                                                                                                        540
gtgbagggta tratcatora degageegee tactteggta tetatgacae tgeaaaaggga
                                                                                                                                        600
atgetteegg atceeaagaa caeteacate gteateaget ggatgatege acagaetgte
                                                                                                                                        药医贝
actigations of configurations are properties and action of the configuration of the configura
                                                                                                                                        720
                                                                                                                                        780
cagticaggge geaaaggaac tgacatcatg tacacaggea egettgactg etggeggaag
                                                                                                                                        340
attgottogtg atgaaggagg caaagotttt ttoaagggtg catggtocaa tgttottoaga
                                                                                                                                        3 17
ggoatgygeg gtgoetttgt gottgtottg tatgatgaaa toaagaagta cacataa -
            <210> 3
           < 111> 997
            <0113> DNA
            <213> Homo sapien
            <400> 3
atgaogghad aggocatoto ottogocasa gaottottgg doggaggdat dgddgddgdd-
                                                                                                                                         4.73
anchocawiga oggoogtigdo toogatogag oggittoaago tigotigotigda gigtiobagoad
                                                                                                                                        12.0
godagdawyd agatogodgo ogadaagdag tabaagggda togtoggabtg dattgtoogd
                                                                                                                                        1 a 0
atococcasgo agoagggogt gotgtootto toggaggggda acotttgcdaa ogtcattogo
                                                                                                                                        240
tabttbbrock obcaagboot daadtbbgco tbbaaggata agtabaagga gatdttbbtg
                                                                                                                                        3.10
ggggggtgg acaagdadad gdagttotgg aggtadtttg ogggdaacdt ggddtodggd
                                                                                                                                        31.0
ggegoggiog grgogadoto dototgoteo gegtadoogo tygattetigo dagaadoogo
                                                                                                                                        4. 0
obggoagugu angbgggaaa guuaggoada gagogogagt boogaggoob gggagachbgo
                                                                                                                                        4 \times 0
obggtgaaga beadcaagte egaeggeate eggggeetgt accagggett eagtgtetee
                                                                                                                                        540
gtgeagggea teatesteta degggegged taetteggeg tgtaegatae ggeeaaggge
                                                                                                                                        500
                                                                                                                                        560
atgeteneng andecaagaa daogdadato gtggtgaget ggatgatege geagaeegtg
abggeogtigg enggegtiggt geobladded thegaeabgg tgoggeggog batgatgatg
                                                                                                                                        7.10
cagtoogggo gcaaaggago tgacatcatg tabaogggca cogtogabtg ttggaggaag
                                                                                                                                        730
atottcagag atgaggggg caaggoottc ttcaagggtg ogtggtccaa cgtcctgcgg
                                                                                                                                        §4 ()
                                                                                                                                        397
ggcatggggg gegesttegt getggteetg taegaegage teaagaaggt gatetaa-
            <210>4
            <111> 43
            <0.10>0.00
            <013> PCRArtificial Sequence
            <.129>
            <D23> PCR Primer
            <400> 4
                                                                                                                                          4.3
ttatatotog agtatgggtg atcacgottg gagottocta aag
            <210> %
            <211> 43
            <.112> DNA
            <213> PCRArtificial Sequence
            <400> 5
tatataggta orttagadat attititgat dicatdatad aad
                                                                                                                                          43
```

<210> €

	<211> 43	
	<211> TS <211> DNA	
	<213> PCRArtificial Sequence	
	<400> 6	
ttatat	ctog agtatgadag atgoogotgt gtoottogod aag	43
	<210> 7	
	<211> 43	
	<212> DNA	
	<213> PCRArtificial Sequence	
	<400> 7	
tatata	aggta cottatgtgt acticitigat ticatcatac aag	413
	<210> 8	
	<211> 43	
	<212> DNA	
	<213> PCRArtificial Sequence	
	<400> 8	
ttatat	ong agtatgangg aacaggneat otenttoged aaa	· <b>1</b> 3
	<010> 9	
	<212> 44	
	<212> DNA	
	<213> PCRArtificial Sequence	
	<400> 3	
tatata	aggta dittagagto accitotiga gotigiogia dagg	44
	3	
	<210> 10	
	<211> 21	
	<212> DNA	
	<213> Artificial Sequence	
	<220>	
	<223> Sequence primer	
	-	
	<400> 10	
t > t < a		21
tatge	catag catttttatc c	دند
	<210> 11	
	<#11> 18	
	<did> DNA</did>	
	<pre><j13> Artificial Sequence</j13></pre>	
	•	
	<400> 11	
c~c~:		18
cycca	aason godaagot	Τ.
	<.110> 12	
	<211> 45	
	<d12> DNA</d12>	

	<220>	
	<.NN3> Mutagenic oligonucleotide primer	
	<400> 12	
ggagat	ggdd tgitidgida iddialogid alogidgiad agaid	45
	<110> 13	
	<211> 45	
	<d1d> DNA</d1d>	
	<_13> Artificial Sequence	
	<4:0)> 13	
		45
340003	enng degatgatgatgatgatgagggood coloo	• -
	<	
	<311> 35	
	<pre>ALT &gt; EMA</pre>	
	<pre>&lt;.:::&gt; Artificial Sequence</pre>	
	<>	
	kiiii > FCR primer	
	<4.10> 14	35
tucggg	gaar tongangang gaadaggoda totoo	33
	<0.10 > 15	
	<0.11> 34	
	<d1u> DNA</d1u>	
	<pre>&lt;.:1&gt;&gt; Artificial Sequence</pre>	
	<4.00> 15	
cccggg	utog agitagagto accititiga goto	34
	<010> 16	
	<pre><d11> 41 <d12> DNA</d12></d11></pre>	
	<pre><!--!!--> Artificial Sequence</pre>	
	<pre><!-- Sequence</pre--></pre>	
	(4.1) > 16	
		41
_		
	<210> 17	
	<pre></pre>	
	<pre><iiiii> PMA</iiiii></pre>	
	<pre><ul> &gt; Artificial Sequence</ul></pre>	
	editts 17	12
ıtaaag	arth othagatoad offoffgago togtogtada g	41
	<2.10× 18	
	all 15 13	
	KARLE DNA	
	<.:13> Artificial Sequence	
	•	
	2200S	

<220%

<223> Sequencing	g primer	
<400> 18		
aaatgataac catctege		18
<210> 19		
<211> 18		
<212> DNA		
<213> Antificial	Sequence	
	•	
<4(0)> 1)		
adttcaagga gaatttcc		18
<210> 00		
<211> 18		
<212> IMA		
<21'> Artificial	. Sequence	
<4(17>-20		
acttogects caeggata		18
<210> 11		
<211> 18		
SZIJA TONA		
<213> Artificial	. Sequence	
<400> 111		
		18
tacggccaag ggcattet		10
<210> 12		
<211> 18		
<210> DNA		
<213> Artificial	Sequence	
	•	
<400> 22		
tgaagoqqaa gricotat		18
<d1.0> 1.3</d1.0>		
<2.1.1.> 1.5		
⊲D1D> DNA		
<pre>&lt;13&gt; Artificial</pre>	Sequence	
• 6		
<400> 23		18
atgooggite oegtaoga		TC
<010> 04		
<2115 /1		
sullity DNA		
<pre></pre> <pre></pre> <pre></pre> <pre>Artificial</pre>	Sequence	
ALL OF ALCIETOTAL	. Objaction	
<220>		
	oligonucleotide primer	
<400 → 24		
ggeolyttoc gtoatottat	cgtcatcgtc g	3 1

<210>	25				
<211>	31				
<212>	DNA				
<213>	Artificial Sequence				
	•				
<400>	25				
	gataagatga cggaacaggc c	3			3:
-555	,	-			
<210>	26				
<211>					
<012>					
	Artificial Sequence				
<2110×	Artificial Sequence				
<220>					
	Fu3D maniman				
<223>	FCR primer				
* 4	0.5				
<400>			_		
ttaaagaatt o	catgaoggaa caggocatot o	cottogodaa -	a		4.3
<010>					
<211>					
<212>					
<213>	Artificial Sequence				
< 4 () .) >					
ttataggate d	ottagatoad ottottgago t	togtogtada (	g		4.1
<210>	⊒A .				
<211>	42				
<212>	DNA				
<213>	Artificial Sequence				
<400>	28				
ttaatgggta d	ccatgacgga acaggecate t	tdottogdda 4	aa		42
<210>	29				
<211>	4.2				
<212>	DNA				
	Artificial Sequence				
<:100>	graph (Control of the Control of the				
	gthagateac ettettgage t	rodiodiaca (	aa		42
ceacasesga	j. lagacoae occorrigajo e	e e ge e ge a e a	99		
<210>	3.5				
<211>					
<111>					
<3>	Artificial Sequence				
<220>					
	Symthetic mal-massis-				
< 5 = 5 >	synthetic polypeptide				
1					
<400>			Tria Ala Dha	Dho	
= '	Lys Ile Phe Arg Asp Gl		nys Ala Phe		
1	5	10		15	

<210> 31 <211> 297

7

```
<212 > PRT
     <213 > Homo sapien
     <400> 31
Met Gly Asp His Ala Trp Ser Phe Leu Lys Asp Fhe Leu Ala Gly Ala
                           10
Val Ala Ala A'a Val Ser Lys Thr Ala Val Ala Fro Ile Glu Arg Val
     2.0
                               25
Lys Leu Leu Leu Gln Val Gln His Ala Ser Lys Gln Ile Ser Ala Glu
                                              45
                           -10
Lys Gln Tyr Lys Gly Ile Ile Asp Cys Val Val Arg Ile Pro Lys Glu
Gin Gly Phe Leu Ser Phe Trp Arg Gly Asn Leu Ala Asn Val Ile Arg
                                       75
                   70
Twr Pha Fro Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys
                                   90
Gln Lew Fhe Leu Gly Gly Val Asp Arg His Lys Gln Phe Trp Arg Tyr
          1.20
                                       110
                               1.05
Phe Ala Gly Am Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu
                          120
Cys Pho Val Tyr Pro Leu Asp Phe Ala Arg Thr Arg Weu Ala Ala Asp
                       135
                                           14.0
Val Gly Ang Ang Ala Gln Ang Glu Phe His Gly Leu Gly Asp Dys Ile
                  150
                                      1.5.5
The Lys The Phe Lys Ser Asp Gly Leu Arg Gly Leu Tyr Gln Gly Phe
                                  170
                                                      175
               165
Ash Val Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Ala Tyr Phe Gly
                              135 130
Val Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Val His
                           200
                                              205
       195
Ile Phe Val Ser Trp Met Ile Ala Gln Ser Val Thr Ala Val Ala Gly
                       215
Leu Lei Ser Tyr Pro Phe Asp Thr Val And And And Met Met Met 31n
                   230
                                       235
Ser Gly Ang Lys Gly Ala Asp Ile Met Tyr Thr Gly Thr Val Asp Gys
                                  250
Trp Ary Lys Ite Ala Lys Asp Glu Gly Ala Lys Ala Phe Phe Lys Gly
                               2.65
Ala Trp Ser Ash Val Leu Arg Bly Met Gly Bly Ala Phe Val Leu Val
                           230
Leu Tyr Asp Glu Ile Lys Lys Tyr Val
    290
                      295
     3.21d> 3.
      <.111> 2 +3
      <...12> PET
     <:113> Homo sapien
     <400> 31
Met Thr Asp Ala Ala Leu Ser Phe Ala Lys Asp Phe Leu Ala Bly Bly
                                  10
Val Ala Ala Ala Ile Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val
```

. .

8

Lys Leu Leu Gln Val Gln His Ala Ser Lys Gln Ile Thr Ala Asp 4.0 Lys Gln Tyr Lys Gly Ile Ile Asp Cys Val Val Arg Ile Fro Lys Glu 55 50 Gln Glu Val Leu Ser Phe Trp Arg Gly Asn Leu Ala Asn Val fle Arg 70 75 50, Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys 95 90 Gln Ile Phe Leu Gly Gly Val Asp Lys Arg Thr Gln Phe Trp Arg Tyr 105 Phe Ala Gly Asn Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu 120 Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg Thr Arg Leu Ala Ala Asp 135 140 Val Gly Lys Ala Gly Ala Glu Arg Glu Phe Arg Bly Leu Gly Asp Cys 150 155 Leu Val Lys lie Tyr Lys Sor Asp Gly Ile Lys Gly Leu Tyr Gln Gly 1.65 170 1.75 Phe Ash Val Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Ala Tyr Phe 140 185 Gly lle Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Thr 205 1.5 His Ile Val Ile Sor Trp Met Ile Ala Gin Thr Val Thr Ala Val Ala 215 220 Gly Leu Thir Ser Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met Met 230 235 225 Gin Ser Gly Arg Lys Gly Thr Asp Ile Met Tyr Thr Gly Thr Leu Asp 245 250 Cys Trp Arg Lys Ile Ala Arg Asp Blu Gly Gly Lys Ala Fhe Phe Lys **165** 1143-0 Gly Ala Trp Ser Ash Val Leu Arg Gly Met Gly Gly Ala Phe Val Leu 280 Val Leu Tyr Asp Glu Ile Lys Lys Tyr Thr 290 2.35 <210> 33 <2115 B \*8 <2115 PRT <21 -> Homo sapien <400> 33 Met Thr Glu Gln Ala Ile Ser Phe Ala Lys Asp Phe Leu Ala Gly Gly 1-0 Ile Ala Ala Ala Ile Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val 25 23 1 Lys Leu Lau Lau 31n Val Gin His Ala Ser Lys Gln Il≏ Ala Ala Asp 3.5 40 4.5 Lys 3ln Tyr Lys 3ly Ile Val Asp Cys Ile Val Arg Ile Pro Lys Glu 55 60 Gln Gly Val Leu Ser Phe Trp Arg Gly Asn Leu Ala Asn Val Ile Arg 7.0 75 Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys

**9** 0

Gln lle Phe Leu Bly Gly Val Asp Lys His Thr Bln Phe Trp Arg Tyr

110 100 100 105 125 120 120 120 120 120 120 120 120
Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg 140  Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg 140  135  130  130  140  160
Val Gly Lys Ser Gly Thr Glu Arg 5 155  150  145  Leu Val Lys Ile Thr Lys Ser Asp Gly Ile Arg Gly Leu Tyr Gln Gly  175  Leu Val Lys Ile Thr Lys Ser Asp Gly Ile Arg Gly Leu Tyr Gln Gly  175  170  180  Phe Ser Val Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Ala Tyr Phe  180  Gly Val Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Thr  205  200  200  Ala Gln Thr Val Thr Ala Val Ala
His Ile Val Val Ser Trp Met Ile Ard Offi 220  His Ile Val Val Ser Trp Met Ile Ard Offi 220  220  215  220  240
Gly Val Val Ser Tyr Pro Phe Asp 235 230 230 230 230 230 245 Gln Ser Gly Arg Lys Gly Ala Asp Ile Met Tyr Thr Gly Thr Val Asp 255 245 Cys Trp Arg Lys Ile Phe Arg Asp Glu Gly Gly Lys Ala Phe Phe Lys 270 265 265 Gly Ala Trp Ser Asn Val Leu Arg Gly Met Gly Gly Ala Phe Val Leu 285
Gly Ala Trp Ser Ash Val 280 275 Val Leu Tyr Asp Glu Leu Lys Lys Val 11e 290 290